

Life Sciences Reporting Summary

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For further information on the points included in this form, see [Reporting Life Sciences Research](#). For further information on Nature Research policies, including our [data availability policy](#), see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

► Experimental design

1. Sample size

Describe how sample size was determined.

The sample size was chosen based on feasibility and literature precedence for similar experiments. Sample sizes are reported in figure legends.

2. Data exclusions

Describe any data exclusions.

Larvae without inflated swimming bladder or no locomotor activity were excluded based on literature precedence for similar experiments

3. Replication

Describe whether the experimental findings were reliably reproduced.

All experiments contain minimum of biological replicates and technical replicates. All results from replicates are consistent.

4. Randomization

Describe how samples/organisms/participants were allocated into experimental groups.

Zebrafish animals were collected from natural crosses, pooled and distributed into multiwell plates, genotyped post recording.

5. Blinding

Describe whether the investigators were blinded to group allocation during data collection and/or analysis.

Data analysis were carried out with Matlab scripts or instrument programs. Therefore, investigators were not blinded to group allocation or analysis of the outcome.

Note: all studies involving animals and/or human research participants must disclose whether blinding and randomization were used.

6. Statistical parameters

For all figures and tables that use statistical methods, confirm that the following items are present in relevant figure legends (or in the Methods section if additional space is needed).

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement (animals, litters, cultures, etc.)
- ☐ ☒ A description of how samples were collected, noting whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ A statement indicating how many times each experiment was replicated
- ☐ ☒ The statistical test(s) used and whether they are one- or two-sided (note: only common tests should be described solely by name; more complex techniques should be described in the Methods section)
- ☐ ☒ A description of any assumptions or corrections, such as an adjustment for multiple comparisons
- ☐ ☒ The test results (e.g. P values) given as exact values whenever possible and with confidence intervals noted
- ☐ ☒ A clear description of statistics including central tendency (e.g. median, mean) and variation (e.g. standard deviation, interquartile range)
- ☐ ☒ Clearly defined error bars

See the web collection on [statistics for biologists](#) for further resources and guidance.

► Software

Policy information about [availability of computer code](#)

7. Software

Describe the software used to analyze the data in this study.

Data was analyzed with Fiji version1.0/ImageJ (NIH), Matlab 20016a and Graphpad Prism7.

For manuscripts utilizing custom algorithms or software that are central to the paper but not yet described in the published literature, software must be made available to editors and reviewers upon request. We strongly encourage code deposition in a community repository (e.g. GitHub). *Nature Methods* [guidance for providing algorithms and software for publication](#) provides further information on this topic.

► Materials and reagents

Policy information about [availability of materials](#)

8. Materials availability

Indicate whether there are restrictions on availability of unique materials or if these materials are only available for distribution by a for-profit company.

All materials are available upon request.

9. Antibodies

Describe the antibodies used and how they were validated for use in the system under study (i.e. assay and species).

All antibodies used are from commercial sources, verified by manufacture quality control. Catalog numbers described in methods section.

10. Eukaryotic cell lines

a. State the source of each eukaryotic cell line used.

HEK293T cells were obtained from ATCC through UC Berkeley Cell Culture Facility.

b. Describe the method of cell line authentication used.

Cells were authenticated by ATCC and UC Berkeley Cell Culture Facility.

c. Report whether the cell lines were tested for mycoplasma contamination.

Cells were tested for mycoplasma by UC Berkeley Cell Culture Facility.

d. If any of the cell lines used are listed in the database of commonly misidentified cell lines maintained by [ICLAC](#), provide a scientific rationale for their use.

No commonly misidentified cell lines were used.

► Animals and human research participants

Policy information about [studies involving animals](#); when reporting animal research, follow the [ARRIVE guidelines](#)

11. Description of research animals

Provide details on animals and/or animal-derived materials used in the study.

Zebrafish Embryos or larvae from 2-6 days post fertilization of the AB and TL strains were used in this study. Sex determination is not applicable at these stages. The following mutants or transgenic lines were used: Calamitygw71 mutants (Calgw71), nacre/mitfa(-/-) mutants, Tg(elavl3:GCaMP5), Tg(dhb:mCherry), and Tg(dhb:eGFP).

Policy information about [studies involving human research participants](#)

12. Description of human research participants

Describe the covariate-relevant population characteristics of the human research participants.

The study did not involve human research participants.

